Figure 1

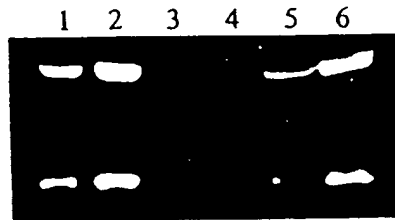## Figure 2

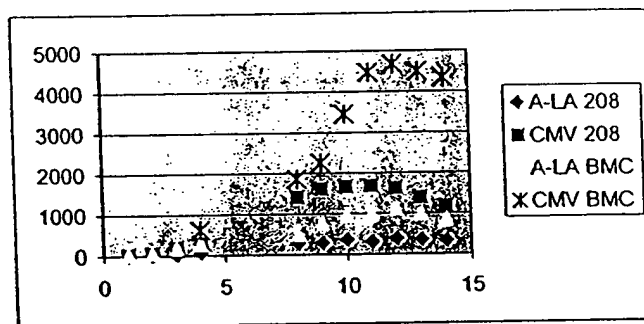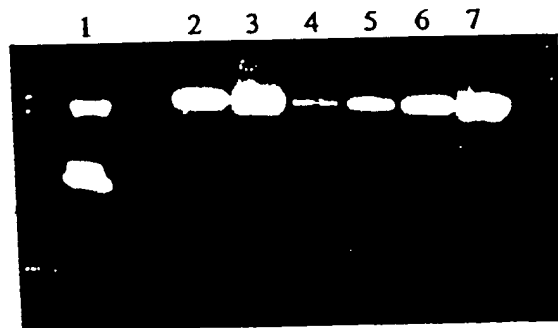## Figure 3

Figure 4
SEQ ID NO:1
Hybrid Human-Bovine Alpha-Lactalbumin Promoter

```
1      GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201    AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251    GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301    CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351    AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401    AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451    AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501    ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551    GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601    CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651    CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701    GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751    CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851    ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
900    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951    ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001   CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051   TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101   CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151   CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201   CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251   GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301   GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501   TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551   TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651   AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701   ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751   CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801   GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851   GACTAGATACTGGGAGAGGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951   CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001   GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051   GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGGGGGGGCCCGGTAC
2101   C
```

1 - 1525	Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)
1526 - 2056	Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)
2057 - 2101	Multiple cloning site

Figure 5
SEQ ID NO:2
Mutated PPE Sequence

```
1      GATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCT
51     ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCG
101    GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151    GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201    AGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
```

1 - 119   Mutated PPE
120 -126   Linker
127 - 245   Mutated PPE

Figure 6
SEQ ID NO:3
IRES-Signal Peptide Sequence

```
  1    GGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
 51    CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101    TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151    ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201    GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251    CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301    AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351    GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401    AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451    GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501    ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551    ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTCTC
601    TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651    GATATCTAGATCTCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 640	Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680	Multiple cloning site

Figure 7a
SEQ ID NO:4
CMV MN14 Vector

```
   1  CGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAA
  51  TATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACA
 101  TTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTG
 151  ACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATA
 201  TATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGAC
 251  CGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATA
 301  GTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACG
 351  GTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGC
 401  CCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAG
 451  TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGT
 501  CATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTG
 551  GATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC
 601  AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCG
 651  TAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGG
 701  AGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA
 751  CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAG
 801  CCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCA
 851  CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
 901  GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
 951  TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCA
1001  CATATTGGATGAGTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
1051  ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
1101  AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
1151  TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
1201  AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
1251  GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
1301  CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
1351  GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
1401  CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
1451  TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
1501  CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
1551  CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
1601  GCCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
1651  AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
1701  GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
1751  TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
1801  TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
1851  CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
1901  CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
1951  CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
2001  GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
2051  TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
2101  CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
2151  GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
2201  ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
2251  GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTA
2301  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
2351  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
2401  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
2451  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
2501  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
2551  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
2601  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
2651  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
2701  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
2751  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAAACGTCTAGGCCCC
2801  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
```

Figure 7b

```
2851   CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
2901   GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
2951   TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
3001   TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
3051   TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
3101   TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
3151   TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
3201   GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
3251   CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
3301   GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
3351   GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
3401   CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
3451   CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
3501   CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
3551   TAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCC
3601   AGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCT
3651   TAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGA
3701   GAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAA
3751   ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
3801   GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
3851   CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
3901   CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC
3951   CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCG ·
4001   CTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAAC
4051   CCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCC
4101   GTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTG
4151   TTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTC
4201   TTTCATT
```

1 ÷ 812	CMV promoter/enhancer
853-855	MN14 antibody heavy chain gene signal peptide start codon
2257 - 2259	MN14 antibody heavy chain gene start codon
2271 - 2846	EMCV IRES
2847 - 2849	Bovine alpha-lactalbumin signal peptide start codon
2904 - 2906	First codon mature MN14 antibody light chain gene
3543 - 3544	MN14 antibody light chain gene stop codon
3614 - 4207	MoMuLV 3' LTR

Figure 8a
SEQ ID NO:5
CMV LL2 Vector

```
1     GGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAAT
51    ATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACAT
101   TTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGA
151   CTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATAT
201   ATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
251   GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG
301   TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGG
351   TAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
401   CCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGT
451   ACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTC
501   ATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGG
551   ATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCA
601   ATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGT
651   AACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGA
701   GGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGAC
751   GCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGC
801   CTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCAC
851   CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
901   TCCACTCCCAGGTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCT
951   GGGTCATCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACCTTTACTAG
1001  CTACTGGCTGCACTGGGTCAGGCAGGCACCTGGACAGGGTCTGGAATGGA
1051  TTGGATACATTAATCCTAGGAATGATTATACTGAGTACAATCAGAACTTC
1101  AAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACAT
1151  GGAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTTTGTGCAA
1201  GAAGGGATATTACTACGTTCTACTGGGGCCAAGGCACCACGGTCACCGTC
1251  TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
1301  CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
1351  ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC
1401  GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT
1451  CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA
1501  TCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
1551  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC
1601  TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG
1651  ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
1701  GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
1751  GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
1801  CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT
1851  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT
1901  CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
1951  ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG
2001  ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA
2051  GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
2101  ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
2151  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCT
2201  GCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAA
2251  AGCCGAATTCGCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAG
2301  CCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCA
2351  TATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTC
2401  TTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGG
2451  TCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGAC
2501  AAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGC
2551  GACAGGTGCCTCTGCGGCCAAAAAGCCACGTGTATAAGATACACCTGCAAA
2601  GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
2651  TCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAG
2701  AAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTT
2751  TACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACG
2801  GGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGT
```

Figure 8b

```
2851  CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC
2901  AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGTTGGAGATAGGGTC
2951  ACTATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTGCAAATCACAA
3001  GAACTACTTGGCCTGGTACCAGCAGAAACCAGGGAAAGCACCTAAACTGC
3051  TGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTTCGCGATTCTCT
3101  GGCAGCGGATCTGGGACAGATTTTACTTTCACCATCAGCTCTCTTCAACC
3151  AGAAGACATTGCAACATATTATTGTCACCAATACCTCTCCTCGTGGACGT
3201  TCGGTGGAGGGACCAAGGTGCAGATCAAACGAACTGTGGCTGCACCATCT
3251  GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTC
3301  TGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
3351  GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACA
3401  GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCT
3451  GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
3501  ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
3551  TAGAGATCTAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATT
3601  TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCA
3651  AGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTG
3701  AGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATA
3751  TGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGC
3801  CAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA
3851  AGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG
3901  GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCC
3951  CCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC
4001  GCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAG
4051  CCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCC
4101  GGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGG
4151  TCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAG
4201  GTCTTTCATT
```

1 - 812	CMV promoter/enhancer
852 - 854	LL2 antibody heavy chain signal peptide start codon
2247 - 2249	LL2 antibody heavy chain stop codon
2261 - 2836	EMCV IRES
2837 - 2839	Bovine alpha-lactalbumin signal peptide start codon
2894-2896	First codon of mature LL2 antibody light chain gene
3551 - 3553	LL2 antibody light chain gene stop codon
3622 - 4210	MoMuLV 3' LTR

```
1     CGAGCTTGGCAGAAATGGTTGAACTCCCGAGAGTGTCCTACACCTAGGGG
51    AGAAGCAGCCAAGGGGTTGTTTCCCACCAAGGACGACCCGTCTGCGCACA
101   AACGGATGAGCCCATCAGACAAAGACATATTCATTCTCTGCTGCAAACTT
151   GGCATAGCTCTGCTTTGCCTGGGGCTATTGGGGGAAGTTGCGGTTCGTGC
201   TCGCAGGGCTCTCACCCTTGACTCTTTCAATAATAACTCTTCTGTGCAAG
251   ATTACAATCTAAACAATTCGGAGAACTCGACCTTCCTCCTGAGGCAAGGA
301   CCACAGCCAACTTCCTCTTACAAGCCGCATCGATTTTGTCCTTCAGAAAT
351   AGAAATAAGAATGCTTGCTAAAAATTATATTTTTACCAATAAGACCAATC
401   CAATAGGTAGATTATTAGTTACTATGTTAAGAAATGAATCATTATCTTTT
451   AGTACTATTTTTACTCAAATTCAGAAGTTAGAAATGGGAATAGAAAATAG
501   AAAGAGACGCTCAACCTCAATTGAAGAACAGGTGCAAGGACTATTGACCA
551   CAGGCCTAGAAGTAAAAAAGGGAAAAAAGAGTGTTTTTGTCAAAATAGGA
601   GACAGGTGGTGGCAACCAGGGACTTATAGGGGACCTTACATCTACAGACC
651   AACAGATGCCCCCTTACCATATACAGGAAGATATGACTTAAATTGGGATA
701   GGTGGGTTACAGTCAATGGCTATAAAGTGTTATATAGATCCCTCCCCTTT
751   CGTGAAAGACTCGCCAGAGCTAGACCTCCTTGGTGTATGTTGTCTCAAGA
801   AAAGAAAGACGACATGAAACAACAGGTACATGATTATATTTATCTAGGAA
851   CAGGAATGCACTTTTGGGGAAAGATTTTCCATACCAAGGAGGGGACAGTG
901   GCTGGACTAATAGAACATTATTCTGCAAAAACTTATGGCATGAGTTATTA
951   TGATTAGCCTTGATTTGCCCAACCTTGCGGTTCCCAAGGCTTAAGTAAGT
1001  TTTTGGTTACAAACTGTTCTTAAAACAAGGATGTGAGACAAGTGGTTTCC
1051  TGACTTGGTTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTTCTATT
1101  TTCCTATGTTCTTTTGGAATTTATCCAAATCTTATGTAAATGCTTATGTA
1151  AACCAAGATATAAAAGAGTGCTGATTTTTTGAGTAAACTTGCAACAGTCC
1201  TAACATTCACCTCTTGTGTGTTTGTGTCTGTTCGCCATCCCGTCTCCGCT
1251  CGTCACTTATCCTTCACTTTCCAGAGGGTCCCCCCGCAGACCCCGGCGAC
1301  CCTCAGGTCGGCCGACTGCGGCAGCTGGCGCCCGAACAGGGACCCTCGGA
1351  TAAGTGACCCTTGTCTTTATTTCTACTATTTTGTGTTCGTCTTGTTTTGT
1401  CTCTATCTTGTCTGGCTATCATCACAAGAGCGGAACGGACTCACCTCAGG
1451  GAACCAAGCTAGCCCGGGGTCGACGGATCCGATTACTTACTGGCAGGTGC
1501  TGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTC
1551  GACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGA
1601  GATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAA
1651  CATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGG
1701  ACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCAC
1751  CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
1801  TCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACCT
1851  GGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCAC
1901  ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGA
1951  TTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCTA
2001  AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCCT
2051  GCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCAA
2101  GCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCCG
2151  GTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
2201  ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG
2251  TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
2301  CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACT
2351  CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC
2401  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
2451  AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTG
2501  CCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAA
2551  AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
2601  GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
2651  GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
2701  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAC
2751  TGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
2801  AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
```

Figure 9b

```
2851  CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG
2901  GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
2951  GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
3001  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
3051  GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
3101  CGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCG
3151  GGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTAC
3201  TGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTAT
3251  TTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGC
3301  CCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGG
3351  AATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTT
3401  CTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCC
3451  CCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC
3501  ACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTG
3551  TGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAG
3601  GATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTG
3651  CACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCC
3701  CGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGC
3751  CTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGG
3801  CCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGT
3851  GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGT
3901  AGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACT
3951  GGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGGT
4001  AGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACAT
4051  CGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAAG
4101  GGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATC
4151  TTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTG
4201  CCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
4251  ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
4301  AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGC
4351  AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
4401  TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATCC
4451  CCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGGA
4501  TTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTT
4551  TTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCT
4601  TCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTC
4651  TCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCA
4701  CTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGT
4751  CAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGA
4801  ACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGG
4851  GCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGG
4901  CTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTA
4951  CGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGC
5001  CGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGG
5051  ATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGATA
5101  AAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCC
5151  CACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCAT
5201  GGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACA
5251  GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
5301  CTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA
5351  ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
5401  GATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
5451  GATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTG
5501  AACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCC
5551  CGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCC
5601  GATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAG
5651  TTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGT
5701  GATTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 1457   Mouse mammary tumor virus LTR

1475 - 1726   Double mutated PPE sequence

Figure 9c

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

```
   1   AAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCA
  51   AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCA
 101   GGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTT
 151   CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
 201   AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAGAA
 251   CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCAT
 301   CAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTTAT
 351   TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCGCT
 401   CTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCT
 451   TCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCTTG
 501   CTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCT
 551   GAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCCGG
 601   GATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAAG
 651   CTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTG
 701   ATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGG
 751   CGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCTGG
 801   GAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAA
 851   GGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGA
 901   GACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGT
 951   TTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
1001   TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGC
1051   CAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGT
1101   CGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
1151   TTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGA
1201   GACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTT
1251   TTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCT
1301   GGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACAC
1351   CCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGA
1401   ACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTC
1451   CTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGATC
1501   GTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTT
1551   GGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGC
1601   TCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTT
1651   TGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAG
1701   CGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTC
1751   GACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCC
1801   GGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCA
1851   TCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
1901   CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGAT
1951   GGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC
2001   TCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGC
2051   GAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGT
2101   GGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGG
2151   CGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAG
2201   CTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGC
2251   TCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
2301   GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGC
2351   CATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTC
2401   GGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCT
2451   CATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGTTGGT
2501   TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2551   AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2601   CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2651   ATCCTAGAACTAGCGAAAATGCAAGAGCAAAGACGAAAACATGCCACACA
2701   TGAGGAATACCGATTCTCTCATTAACATATTCAGGCCAGTTATCTGGGCT
2751   TAAAAGCAGAAGTCCAACCCAGATAACGATCATATACATGGTTCTCTCCA
2801   GAGGTTCATTACTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCCTG
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Figure 10b

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2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCCAATACTTTGGC
2901 CACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTGATACTGGGAAA
2951 GATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAAGAGTTGGATGG
3001 AATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCCAGGAGTTGGTA
3051 ATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTTGCAAAGAGTTG
3101 GACACTACTGAGTGACTGAACTGAACTGATAGTGTAATCCATGGTACAGA
3151 ATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTGAAGAGTTGTAG
3201 GATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTAAATTATTTACT
3251 TAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTTAGAGACTGATG
3301 TAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCTATTGGTTATAG
3351 CTGTTATAACCAATATATAACCAATATATTGGTTATATAGCATGAAGCTT
3401 GATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATCCTAAACTCTAC
3451 ATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAATCTTGTTTTATA
3501 GGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCAGATGGTAAAGT
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGGCTTGGGAAGAT
3601 CCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTTACCTGGAAAAT
3651 TCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGGATTGCAAAGAG
3701 TTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGTATACACCTGTG
3751 AGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGCATTGCAGAAAG
3801 ATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATACTGGAGTGGGT
3851 AGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAATTGAACTGGAG
3901 TCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTACCAGGTGGATA
3951 CTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCACCTTTCCCAAA
4001 AAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACTCTGAGGCTGTC
4051 TACAAGCTTATATATTTATGAACACATTTATTGCAAGTTGTTAGTTTTAG
4101 ATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTGGTTGGGGATGG
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTCATACACACTTT
4201 TCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGATCTAAGTTATAT
4251 GTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCCTGACCACTCAA
4301 CAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCATGCCTGGGTTG
4351 AGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGCTGGATTGGTTG
4401 GACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGATGACATACACC
4451 CCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGGAAGCTCGGTAT
4501 AGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTATATTGCCCCCAT
4551 GCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTCCCAGAACCAAC
4601 CCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAAGCAGGATCATG
4651 GTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATGGACTAGATACT
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGGCAGGC
4751 TCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATTCTCTTCCTAGA
4801 TGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCATGAATATAAATA
4851 TATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGGGCGCCGAATTC
4901 GAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTTACTGGCAGGTG
4951 CTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCT
5001 CGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
5051 AGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGA
5101 ACATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGG
5151 GACGCGGCGGTGGTAATTACAAGCGAGATCCCGGGAATTCAGGACCTCA
5201 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
5251 GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
5301 TGGCCGGTCCCTGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCA
5351 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
5401 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
5451 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
5501 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
5551 AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
5601 GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
5651 CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCCGGCCCTGGGCTGCCTG
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
5751 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
5851 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
5901 CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
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Figure 10c

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5951 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
6001 AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
6051 GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
6101 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
6151 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
6201 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
6251 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
6301 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
6351 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
6401 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
6451 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
6501 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
6551 ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
6601 GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTA
6651 CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
6701 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
6751 CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
6801 GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
6851 TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
6901 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
6951 CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
7001 GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
7051 GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
7101 GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
7151 CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
7201 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
7251 GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
7301 TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
7351 TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
7401 TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
7451 TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
7501 TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
7551 GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
7601 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
7651 GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
7701 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
7751 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
7801 CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
7851 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
7901 CCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGG
7951 ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCT
8001 TTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGC
8051 TTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGT
8101 CTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGC
8151 ACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTG
8201 TCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGG
8251 AACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTG
8301 GGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTG
8351 GCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCT
8401 ACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTG
8451 CCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCG
8501 GATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGAT
8551 AAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACC
8601 CCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCA
8651 TGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAAC
8701 AGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTT
8751 CCTGCCCCGGCTCAGGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCA
8801 AACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAAC
8851 AGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATC
8901 AGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTT
8951 GAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCC
9001 CCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTC
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Figure 10d

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9051   CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCA
9101   GTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAG
9151   TGATTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 658	MoMuSV 5' LTR
659 - 1468	Extended packaging region
1512 - 2306	Neomycin resistance gene
2661 - 4896	Bovine/human alpha-lactalbumin 5' flanking region
5084 - 5327	Double mutated PPE sequence
6207 - 6209	MN14 antibody heavy chain gene signal peptide start codon
6611-6613	MN14 antibody heavy chain stop codon
6625 - 7200	EMCV IRES
7201 - 7203	Bovine alpha-lactalbumin signal peptide start codon
7258 - 7260	First codon of mature MN14 antibody light chain gene
7897 - 7899	MN14 antibody light gene stop codon
7938 - 8529	WPRE sequence
8600 - 9138	Moloney murine leukemia virus 3' LTR

```
   1    GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
  51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
 101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
 151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
 201    AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
 251    GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
 301    CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
 351    AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
 401    AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
 451    AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
 501    ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
 551    GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
 601    CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
 651    CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
 701    GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
 751    CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
 801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
 851    ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
 901    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
 951    ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001    CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051    TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101    CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151    CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201    CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251    GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGTATTGGTG
1301    GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351    ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401    CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451    TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501    TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551    TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601    TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651    AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701    ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751    CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801    GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851    GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901    AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951    CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001    GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051    GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101    ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151    CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201    AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251    GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301    TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGAAGC
2351    TTGTTGGGAATTCAGGCCATCGATCCCGCCGCCACCATGGAATGGAGCTG
2401    GGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCACTCCGACATCC
2451    AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC
2501    ACTATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTA
2551    TCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAA
2601    CCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACA
2651    CAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA
2701    TTACTGTCAACATTTTTGGAGTACTCCGTGGACGTTCGGTGGAGGCACCA
2751    AGCTGGAAATCAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
2801    CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT
```

Figure 11b

2851	GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
2901	GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
2951	GACAGCACCTACAGCATGAGCAGCACCCTCACATTGACCAAGGACGAGTA
3001	TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
3051	CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTGAAAGCATCGATTT
3101	CCCCTGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAA
3151	GCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACC
3201	ATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTT
3251	CTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAG
3301	GTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGA
3351	CAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGG
3401	CGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA
3451	AGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGA
3501	GTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCA
3551	GAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCT
3601	TTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCAC
3651	GGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTG
3701	TCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAGGTT
3751	CAGCTTCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAA
3801	GTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTTTATGCACT
3851	GGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGAT
3901	CCTGCGAATGGGAATACTGAATATGACCCGAAGTTCCAGGGCAAGGCCAC
3951	TATAACAGCAGACACATCCTCCAACACAGTCAACCTGCAGCTCAGCAGCC
4001	TGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGTGGAGGGGAACTG
4051	GGGTTTCCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCAGCCAA
4101	AACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAA
4151	CTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAG
4201	CCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACAC
4251	CTTCCCAGCTGTCCTGCAGTTTGACCTCTACACTCTGAGCAGCTCAGTGA
4301	CTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCC
4351	CACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTG
4401	TACTAGTGGAGGTGGAGGTAGCCACCACCATCACCATTAATCTAGAG
4451	TTAAGCGGCCGTCGAGATCTCGACATCGATAATCAACCTCTGGATTACAA
4501	AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGC
4551	TATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGT
4601	ATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTA
4651	TGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGT
4701	TTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTC
4751	CTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCAT
4801	CGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
4851	ACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTC
4901	GCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCC
4951	TTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTC
5001	TGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCC
5051	CTTTGGGCCGCCTCCCCGCCTGATCGATAAAATAAAAGATTTTATTTAGT
5101	CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
5151	AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
5201	TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
5251	CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
5301	AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
5351	GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
5401	AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
5451	GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
5501	CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
5551	CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
5601	ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC

Figure 11c

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5651   GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
5701   GGTCTTTCATT
```

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mtated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

```
1     TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51    TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAGTTCAGATCAAG
101   GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151   GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201   GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
251   AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301   TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
351   TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
401   CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
451   GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
501   CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
551   CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
601   CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
651   TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
701   TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751   CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
801   CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
851   GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901   AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
951   CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCCAAGCTTGGGC
1001  TGCAGGTCGAGGACTGGGGACCCTGCACCGAACATGGAGAACACAACATC
1051  AGGATTCCTAGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTTGTTGA
1101  CAAGAATCCTCACAATACCACAGAGTCTAGACTCGTGGTGGACTTCTCTC
1151  AATTTTCTAGGGGGAGCACCCACGTGTCCTGGCCAAAATTCGCAGTCCCC
1201  AACCTCCAATCACTCACCAACCTCTTGTCCTCCAATTTGTCCTGGCTATC
1251  GCTGGATGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCTA
1301  TGCCTCATCTTCTTGTTGGTTCTTCTGGACTACCAAGGTATGTTGCCCGT
1351  TTGTCCTCTACTTCCAGGAACATCAACTACCAGCACGGGACCATGCAAGA
1401  CCTGCACGATTCCTGCTCAAGGAACCTCTATGTTTCCCTCTTGTTGCTGT
1451  ACAAAACCTTCGGACGGAAACTGCACTTGTATTCCCATCCCATCATCCTG
1501  GGCTTTCGCAAGATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGC
1551  TCAGTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCACT
1601  GTTTGGCTTTCAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTA
1651  CAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTT
1701  GGGTATACATTTAAACCCTAATAAAACCAAACGTTGGGGCTACTCCCTTA
1751  ACTTCATGGGATATGTAATTGGATGTTGGGGTACTTTACCGCAAGAACAT
1801  ATTGTACTAAAAATCAAGCAATGTTTTCGAAAACTGCCTGTAAATAGACC
1851  TATTGATTGGAAAGTATGTCAGAGACTTGTGGGTCTTTTGGGCTTTGCTG
1901  CCCCTTTTACACAATGTGGCTATCCTGCCTTAATGCCTTTATATGCATGT
1951  ATACAATCTAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCT
2001  GTGTAAACAATATCTGAACCTTTACCCCGTTGCCCGGCAACGGTCAGGTC
2051  TCTGCCAAGTGTTTGCTGACGCAACCCCCACTGGATGGGGCTTGGCTATC
2101  GGCCATAGCCGCATGCGCGGACCTTTGTGGCTCCTCTGCCGATCCATACT
2151  GCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGGCGGTCTGGAGCGAAACT
2201  TATCGGCACCGACAACTCTGTTGTCCTCTCTCGGAAATACACCTCCTTTC
2251  CATGGCTGCTAGGGTGTGCTGCCAACTGGATCCCCTCAGGATATAGTAGT
2301  TTCGCTTTTGCATAGGGAGGGGGAAATGTAGTCTTATGCAATACACTTGT
2351  AGTCTTGCAACATGGTAACGATGAGTTAGCAACATGCCTTACAAGGAGAG
2401  AAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTACGATCGTGC
2451  CTTATTAGGAAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTG
2501  AATTCCGCATTGCAGAGATAATTGTATTTAAGTGCCTAGCTCGATACAGC
2551  AAACGCCATTTTTGACCATTCACCACATTGGTGTGCACCTTCCAAAGCTT
2601  CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651  ACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAG
2701  CTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGG
2751  TAGCTTGCAGTGGGCTTACATGGCGATAGCTAGACTGGGCGGTTTTATGG
2801  ACAGCAAGCGAACCGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGG
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Figure 12b

```
2851   GAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGATCTGAT
2901   GGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC
2951   ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA
3001   GAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATG
3051   CCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAG
3101   ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCT
3151   ATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTG
3201   TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG
3251   GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC
3301   TGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCG
3351   ACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCC
3401   GGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC
3451   AGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATC
3501   TCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT
3551   GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCG
3601   CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCG
3651   GCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGAT
3701   TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGG
3751   ACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACG
3801   AGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCG
3851   TTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG
3901   GAGTTCTTCGCCCACCCCAACCCTGGCCCTATTATTGGGTGGACTAACCA
3951   TGGGGGGAATTGCCGCTGGAATAGGAACAGGGACTACTGCTCTAATGGCC
4001   ACTCAGCAATTCCAGCAGCTCCAAGCCGCAGTACAGGATGATCTCAGGGA
4051   GGTTGAAAAATCAATCTCTAACCTAGAAAAGTCTCTCACTTCCCTGTCTG
4101   AAGTTGTCCTACAGAATCGAAGGGGCCTAGACTTGTTATTTCTAAAAGAA
4151   GGAGGGCTGTGTGCTGCTCTAAAAGAAGAATGTTGCTTCTATGCGGACCA
4201   CACAGGACTAGTGAGAGACAGCATGGCCAAATTGAGAGAGAGGCTTAATC
4251   AGAGACAGAAACTGTTTGAGTCAACTCAAGGATGGTTTGAGGGACTGTTT
4301   AACAGATCCCCTTGGTTTACCACCTTGATATCTACCATTATGGGACCCCT
4351   CATTGTACTCCTAATGATTTTGCTCTTCGGACCCTGCATTCTTAATCGAT
4401   TAGTCCAATTTGTTAAAGACAGGATATCAGTGTCCAGGCTCTAGTTTTG
4451   ACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAA
4501   ATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA
4551   CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG
4601   AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGA
4651   TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
4701   GCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAAC
4751   AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
4801   TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA
4851   TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAA
4901   CTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCG
4951   AGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGA
5001   TTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTT
5051   GCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGA
5101   TTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 589	MoMuSV 5' LTR
659 - 897	Retroviral packaging region
1034 - 1714	Hepatitis B surface antigen
2279 - 2595	RSV promoter
2951 - 3745	Neomycin phosphotransferase gene
4537 - 5130	MoMuLV 3' LTR

Figure 13a
SEQ ID NO:10
Alpha-Lactalbumin cc491L2 Vector

```
1     GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101   ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151   GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201   AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251   GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301   CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351   AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401   AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451   AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501   ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551   GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601   CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651   CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701   GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751   CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801   ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851   ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901   ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951   ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAATGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGAAGCTTTAACCATG
2101  GAATGGAGCTGGGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCA
2151  CTCCCAGGTTCAGTTGCAGCAGTCTGACGCTGAGTTGGTGAAACCTGGGG
2201  CTTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTACACCTTCACTGACCAT
2251  GCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGG
2301  ATATTTTTCTCCCGGAAATGATGATTTTAAATACAATGAGAGGTTCAAGG
2351  GCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACTGCCTACGTGCAG
2401  CTCAACAGCCTGACATCTGAGGATTCTGCAGTGTATTTCTGTACAAGATC
2451  CCTGAATATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG
2501  GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGGACATT
2551  GTGATGTCACAGTCTCCATCCTCCCTACCTGTGTCAGTTGGCGAGAAGGT
2601  TACTTTGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTGGTAATCAAA
2651  AGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
2701  CTGATTTACTGGGCATCCGCTAGGGAATCTGGGGTCCCTGATCGCTTCAC
2751  AGGCAGTGGATCTGGGACAGATTTCACTCTCTCCATCAGCAGTGTGAAGA
2801  CTGAAGACCTGGCAGTTTATTACTGTCAGCAGTATTATAGCTATCCCCTC
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Figure 13b

```
2851  ACGTTCGGTGCTGGGACCAAGCTGGTGCTGAAACGGGCCGCCGAGCCCAA
2901  ATCTCCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC
2951  TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
3001  ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
3051  CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
3101  ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
3151  GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA
3201  GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA
3251  CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
3301  CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCT
3351  GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
3401  GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC
3451  GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
3501  GCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC
3551  ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGGAGGCGGATCA
3601  GGAGGTGGCGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAACT
3651  GGAGCATTTACTGCTGGATTTACAGATGATTTTGAATGGAATTAATAATT
3701  ACAAGAATCCCAAACTCACCAGGATGCTCACATTTAAGTTTTACATGCCC
3751  AAGAAGGCCACAGAACTGAAACATCTTCAGTGTCTAGAAGAAGAACTCAA
3801  ACCTCTGGAGGAAGTGCTAAATTTAGCTCAAAGCAAAAACTTTCACTTAA
3851  GACCCAGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACTAAAG
3901  GGATCTGAAACAACATTCATGTGTGAATATGCTGATGAGACAGCAACCAT
3951  TGTAGAATTTCTGAACAGATGGATTACCTTTTGTCAAAGCATCATCTCAA
4001  CACTAACTTGAAGCTTGTTAACATCGATAAAATAAAAGATTTTATTTAGT
4051  CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
4101  AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
4151  TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
4201  CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
4251  AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
4301  GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
4351  AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
4401  GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
4451  CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
4501  CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
4551  ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC
4601  GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
4651  GGTCTTTCATT
```

1 - 2055	Bovine/human alpha-lactalbumin 5' flanking region
2098 - 4011	cc49-IL2 coding region
4068 - 4661	MoMuLV 3' LTR

```
1      GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101    ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201    AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251    GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301    CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351    AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401    AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451    AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501    ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551    GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601    CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651    CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701    GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751    CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851    ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951    ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001   CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051   TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101   CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151   CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201   CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251   GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301   GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501   TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551   TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGGAAGGGGG
1651   AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701   ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751   CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801   GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851   GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951   CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001   GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051   GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101   ACTGGCAGGTGCTGGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151   CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201   AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGGCTTCCGA
2251   GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301   TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGTTAA
2351   CAGATCTAGGCCTCCTAGGTCGACGGATCCCCGGGAATTCGGCGCCGCCA
2401   CCATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCC
2451   ACCCAGGCCCAGGTCCAACTGCAGCAGTCTGGGCCTGAGCTGGTGAAGCC
2501   TGGGACTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAA
2551   GCTACTATTTACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGG
2601   ATTGCATGGATTTATCCTGGAAATGTTATTACTACGTACAATGAGAAGTT
2651   CAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACA
2701   TGCACCTCAACAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCA
2751   AGGGGTGACCATGATCTTGACTACTGGGGCCAAGGCACCACTCTCACAGT
2801   CTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGAT
```

Figure 14b

```
2851  CTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGC
2901  TATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAG
2951  CGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGA
3001  GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACC
3051  TGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
3101  GCCCAGGGATTGTACTAGTGGAGGTGGAGGTAGCTAAGGGAGATCTCGAC
3151  GGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTACTGG
3201  CCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTT
3251  CCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCT
3301  GTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAAT
3351  GCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTT
3401  GAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCA
3451  CCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACC
3501  TGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGG
3551  AAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGAT
3601  GCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCAC
3651  ATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGA
3701  ACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTC
3751  CTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCG
3801  ACATTGTGCTGACACAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAG
3851  AAGGTCACCATGACCTGCAGTGCCACCTCAAGTGTAAGTTACATACACTG
3901  GTACCAGCAGAAGTCAGGCACCTCCCCAAAAGATGGATTTATGACACAT
3951  CCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGG
4001  ACCTCTCACTCTCTCACACTCAGCAGCATGGAGGCTGAAGATGCTGCCAC
4051  TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTCGGTGCGGGGACCA
4101  AGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
4151  CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT
4201  GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
4251  GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
4301  GACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA
4351  TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
4401  CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAATAGGGGAGATCT
4451  CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTG
4501  GTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA
4551  ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTC
4601  CTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTG
4651  TCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACT
4701  GGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTT
4751  CCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCT
4801  GCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCG
4851  GGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT
4901  TCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGG
4951  ACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTT
5001  CGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCC
5051  TGATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAAT
5101  GAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTT
5151  GCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGG
5201  TCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
5251  AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAAT
5301  ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
5351  CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGA
5401  GAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTG
5451  CCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCT
5501  TCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
5551  CAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACC
5601  CTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCT
```

Figure 14c

5651   CCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

Figure 15
SEQ ID NO:12
IRES-Casein Signal Peptide Sequence

```
1     GGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51    CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101   TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151   ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251   CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301   AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351   GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401   AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451   GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501   ATGTGTTTAGTCGAGGTTAAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551   ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTTGCTCATCCT
601   TACCTGTCTTGTGGCTGTTGCTCTTGCCGGCGCCATGGGATATCTAGATC
651   TCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 628	Modified bovine alpha-S1 casein signal peptide coding region
629 - 668	Multiple cloning site

Figure 16a

SEQ ID NO: 13

LNBOTDC Vector

```
   1  TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
  51  TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
 101  GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
 151  GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
 201  GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
 251  AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
 301  TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
 351  TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
 401  CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
 451  GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
 501  CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
 551  CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
 601  CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
 651  TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
 701  TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
 751  CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
 801  CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
 851  GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
 901  AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
 951  CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATC
1001  GTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTA
1051  GGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAG
1101  ATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGT
1151  TGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCC
1201  GCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGG
1251  TCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTG
1301  ACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGT
1351  ACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCC
1401  TTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTC
1451  ACTCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAG
1501  GATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC
1551  GCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGG
1601  CTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTC
1651  TTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAG
1701  GCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGT
1751  GCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAG
1801  TGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTA
1851  TCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC
1901  CTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
1951  GGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAG
2001  GGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGA
2051  CGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCA
2101  TGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGT
2151  GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
2201  AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCG
2251  CCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTC
2301  TTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAAC
2351  CTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGG
2401  CTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGG
2451  ATCTCATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGT
2501  TGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCA
2551  GTGCAAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCC
2601  ATGCCCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAG
2651  GCGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCA
2701  ATATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTAC
2751  ATTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATT
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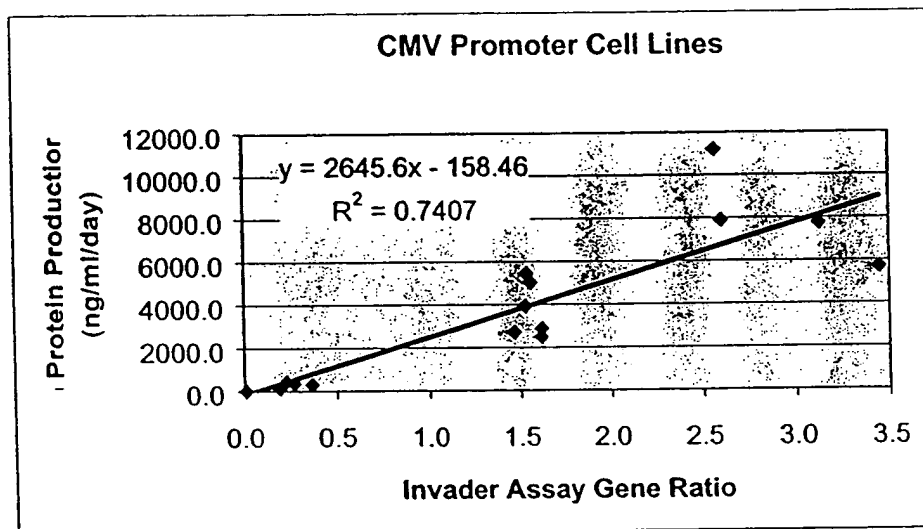
Figure 16b

```
2801  GACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCAT
2851  ATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
2901  CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCAT
2951  AGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTAC
3001  GGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG
3051  CCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCA
3101  GTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAG
3151  TCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGT
3201  GGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGT
3251  CAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTC
3301  GTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGG
3351  GAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAG
3401  ACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCA
3451  GCCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGCCATC
3501  GATCCCGCCGCCACCATGGAATGGAGCTGGGTCTTTCTCTTCTTCCTGTC
3551  AGTAACTACAGGTGTCCACTCCGACATCCAGATGACCCAGTCTCCAGCCT
3601  CCCTATCTGCATCTGTGGGAGAAACTGTCACTATCACATGTCGAGCAAGT
3651  GGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATC
3701  TCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCAT
3751  CAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
3801  AGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAG
3851  TACTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTG
3901  ATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACA
3951  TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGA
4001  CATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCC
4051  TGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC
4101  AGCACCCTCACATTGACCAAGGACGAGTATGAACGACATAACAGCTATAC
4151  CTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCA
4201  ACAGGAATGAGTGTTGAAAGCATCGATTTCCCCTGAATTCGCCCCTCTCC
4251  CTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
4301  GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAAT
4351  GTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGG
4401  TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGG
4451  AAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACC
4501  CTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCA
4551  AAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCC
4601  ACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGC
4651  GTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG
4701  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGT
4751  TAAAAAAACGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGA
4801  AAAACACGATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCA
4851  TCCTATTCCATGCCACCCAGGCCGAGGTTCAGCTTCAGCAGTCTGGGGCA
4901  GAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGG
4951  CTTCAACATTAAAGACACCTTTATGCACTGGGTGAAGCAGAGGCCTGAAC
5001  AGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGGAATACTGAA
5051  TATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTC
5101  CAACACAGTCAACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCG
5151  TCTATTACTGTGCTAGTGGAGGGGAACTGGGGTTTCCTTACTGGGGCCAA
5201  GGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACACCCCCATCTGTCTA
5251  TCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGG
5301  GATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAAC
5351  TCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTC
5401  TGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGC
5451  CCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAG
5501  GTGGACAAGAAAATTGTGCCCAGGGATTGTAACTAGTGGAGGTGGAGGTAG
5551  CCACCATCACCATCACCATTAATCTAGAGTTAAGCGGCCGTCGAGATCTA
5601  GGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAG
5651  AAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTA
5701  AGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGA
5751  AGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAAC
5801  AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
5851  TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
```

Figure 16c

```
5901   GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT
5951   CAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT
6001   GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCT
6051   TCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
6101   CTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGT
6151   GTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTT
6201   CCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTT
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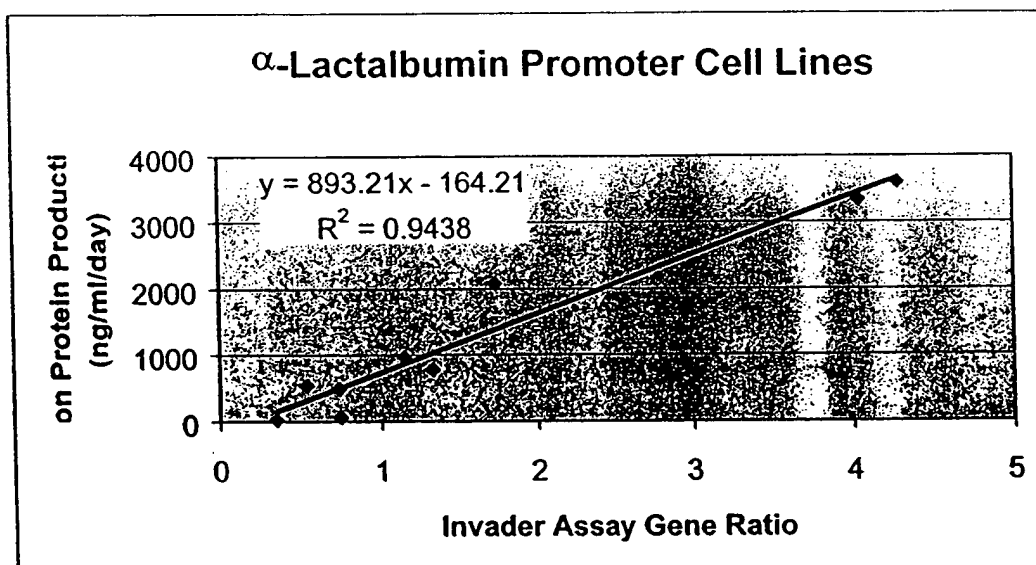
Moloney Murine Sarcoma Virus 5' LTR	1 - 589
Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonetech)	4235 - 4816
Modified Bovine α-LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

Figure 17. CMV construct containing cell lines.

CMV Promoter Cell Lines

$y = 2645.6x - 158.46$

$R^2 = 0.7407$

Protein Production (ng/ml/day)

Invader Assay Gene Ratio

Figure 18: α-Lactalbumin construct containing cell lines

α-Lactalbumin Promoter Cell Lines

$y = 893.21x - 164.21$

$R^2 = 0.9438$

on Protein Producti (ng/ml/day)

Invader Assay Gene Ratio

```
   1  GAATTAATTCATACCAGATCACCGAAAACTGTCCTCCAAATGTGTCCCCC
  51  TCACACTCCCAAATTCGCGGGCTTCTGCCTCTTAGACCACTCTACCCTAT
 101  TCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTT
 151  TGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG
 201  CAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGT
 251  CAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGG
 301  TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGG
 351  CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAG
 401  AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATC
 451  ATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTT
 501  ATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCG
 551  CTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGT
 601  CTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCT
 651  TGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCT
 701  CTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCC
 751  GGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
 801  AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTT
 851  TGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCT
 901  GGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCT
 951  GGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGG
1001  AAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAG
1051  GAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCG
1101  GTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGT
1151  TCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG
1201  GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGAT
1251  GTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTG
1301  GGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGC
1351  GAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTC
1401  TTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGAC
1451  CTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTAC
1501  ACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTT
1551  GAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
1601  TCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGG
1651  AGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATC
1701  ATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAA
1751  CCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCA
1801  ACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAG
1851  CGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATC
1901  ATTTTACTGGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCT
1951  GCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAA
2001  CAGGGGCATCTTGAGCCCCTGCGGACGGTGTCGACAGGTGCTTCTCGATC
2051  TGCATCCTGGGATCAAAGCGATAGTGAAGGACAGTGATGGACAGCCGACG
2101  GCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTA
2151  AGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGAT
2201  TCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGA
2251  CGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCG
2301  CCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAAT
2351  AGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG
2401  TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTACGAGTTGGT
2451  TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2501  AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2551  CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2601  ATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAATAT
2651  TGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTT
2701  ATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGACT
2751  AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATAT
2801  GGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGC
2851  CCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTA
```

Figure 19b

```
2901  ACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTA
2951  AACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCC
3001  CTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTAC
3051  ATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCAT
3101  CGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGAT
3151  AGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
3201  GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAA
3251  CAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGG
3301  TCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGC
3351  CATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCT
3401  CCGCGGCCCCAAGCTTCTCGAGTTAACAGATCTAGGCTGGCACGACAGGT
3451  TTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAG
3501  CTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTAT
3551  GTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
3601  ACCATGATTACGCCAAGCTTGGCTGCAGGTCGACGGATCCACTAGTAACG
3651  GCCGCCAGTGTGCTGGAATTCACCATGGGGCAACCCGGGAACGGCAGCGC
3701  CTTCTTGCTGGCACCCAATGGAAGCCATGCGCCGGACCACGACGTCACGC
3751  AGCAAAGGGACGAGGTGTGGGTGGTGGGCATGGGCATCGTCATGTCTCTC
3801  ATCGTCCTGGCCATCGTGTTTGGCAATGTGCTGGTCATCACAGCCATTGC
3851  CAAGTTCGAGCGTCTGCAGACGGTCACCAACTACTTCATCACAAGCTTGG
3901  CCTGTGCTGATCTGGTCATGGGGCTAGCAGTGGTGCCCTTTGGGGCCGCC
3951  CATATTCTCATGAAAATGTGGACTTTTGGCAACTTCTGGTGCGAGTTCTG
4001  GACTTCCATTGATGTGCTGTGCGTCACGCCATCGATTGAGACCCTGTGCG
4051  TGATCGCAGTCGACCGCTACTTTGCCATTACTAGTCCTTTCAAGTACCAG
4101  AGCCTGCTGACCAAGAATAAGGCCCGGGTGATCATTCTGATGGTGTGGAT
4151  TGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCACTGGTACAGGG
4201  CCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGAC
4251  TTCTTCACGAACCAAGCCTATGCCATTGCCTCTTCCATCGTGTCCTTCTA
4301  CGTTCCCCTGGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGG
4351  CCAAAAGGCAGCTCCAGAAGATTGACAAATCTGAGGGCCGCTTCCATGTC
4401  CAGAACCTTAGCCAGGTGGAGCAGGATGGGCGGACGGGGCATGGACTCCG
4451  CAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCTCAAGACGTTAG
4501  GCATCATCATGGGCACTTTCACCCTCTGCTGGCTGCCCTTCTTCATCGTT
4551  AACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACAT
4601  CCTCCTAAATTGGATAGGCTATGTCAATTCTGGTTTCAATCCCCTTATCT
4651  ACTGCCGGAGCCCAGATTTCAGGATTGCCTTCCAGGAGCTTCTGTGCCTG
4701  CGCAGGTCTTCTTTGAAGGCCTATGGCAATGGCTACTCCAGCAACGGCAA
4751  CACAGGGGAGCAGAGTGGATATCACGTGGAACAGGAGAAAGAAAATAAAC
4801  TGCTGTGTGAAGACCTCCCAGGCACGGAAGACTTTGTGGGCCATCAAGGT
4851  ACTGTGCCTAGCGATAACATTGATTCACAAGGGAGGAATTGTAGTACAAA
4901  TGACTCACTGCTCTCGAGAATCGAGGGGCGGCACCACCATCATCACCACG
4951  TCGACCCCGGGGACTACAAGGATGACGATGACAAGTAAGCTTTATCCATC
5001  ACACTGGCGGCCGCTCGAGCATGCATCTAGCGGCCGCTCGAGGCCGGCAA
5051  GGCCGGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCCTAACGTTA
5101  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
5151  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
5201  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
5251  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
5301  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
5351  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
5401  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
5451  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
5501  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
5551  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
5601  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
5651  CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
5701  GCCGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAG
5751  GGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACA
5801  ATAAGAACTATTTAGCTTGGTATCAGCAGAAACCAGGACAGCCTCCTAAG
5851  CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT
5901  CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC
5951  AGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCAG
```

Figure 19c

```
6001  ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACC
6051  ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTG
6101  CCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
6151  CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT
6201  CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGA
6251  CGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTC
6301  ACCCATCAGGGCCTGAGATCGCCCGTCACAAAGAGCTTCAACAAGGGGAG
6351  AGTGTTAGTTCTAGATAATTAATTAGGAGGAGATCTCGAGCTCGCGAAAG
6401  CTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCG
6451  TTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCCTCCTA
6501  GGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGG
6551  GGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCC
6601  ATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGAT
6651  CAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCT
6701  GTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGC
6751  TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCT
6801  CAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTT
6851  CTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACC
6901  CTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGC
6951  GCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGG
7001  GGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAAT
7051  AAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAG
7101  GGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGG
7151  GGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCAC
7201  CGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACC
7251  TCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
7301  GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTG
7351  TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG
7401  GCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGC
7451  GGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGC
7501  TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG
7551  GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT
7601  CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCC
7651  AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC
7701  CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
7751  CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG
7801  CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCT
7851  CCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA
7901  GTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC
7951  GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA
8001  CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA
8051  TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG
8101  CCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
8151  GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
8201  AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACG
8251  CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC
8301  TGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT
8351  TATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT
8401  AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
8451  CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCA
8501  TAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTA
8551  CCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGC
8601  TCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAA
8651  GTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGG
8701  GAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGC
8751  CATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCAT
8801  TCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG
8851  TGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAA
8901  GTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTC
8951  TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCA
9001  ACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCC
9051  GGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGC
```
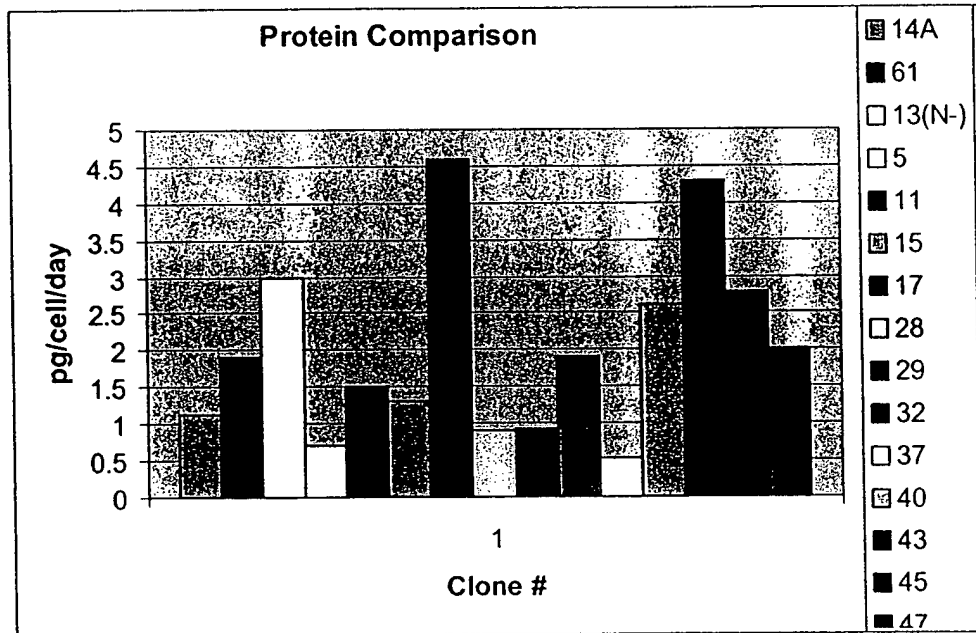
Figure 19d

```
9101   TCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCG
9151   CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC
9201   AGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGC
9251   AAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTC
9301   ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT
9351   CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGG
9401   TTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATT
9451   ATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCG
   1.  TCTTCAAGAAT
```
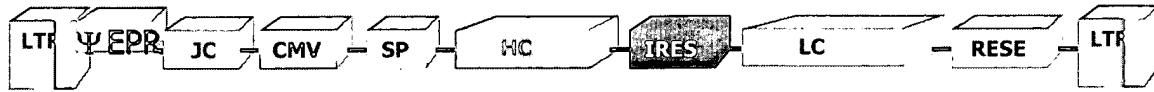
Features:
```
149-737    Moloney murine sarcoma virus 5' LTR
807-1616   Extended Packaging Region
1680-1735  EM7 promoter (bacteriophage T7 promoter)
1754-2151  Blasticidin resistance gene coding sequence
2310-2440  SV40 poly A signal and site
2603-3420  CMV IE promoter
3675-4988  G-protein-coupled receptor (GPCR)
5071-5646  IRES
5647-5703  Bovine a-lactalbumin signal peptide
5704-6372  'humanized' antibody light chain
6553-7146  MoMuLV 3' LTR
7683Origin of replication
9302-8442  b-Lactmase coding sequence
```

Figure 20

Protein Comparison

Figure 21(A). Gene Sequence of a Single Retrovector IgM Construct (SEQ ID NO:37)

LTR =   Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat
                 Fusion
Ψ EPR =   Moloney Murine Leukemia Virus Psi Region and Extended Viral
                 Packaging Region
JC =   J Chain Gene
CMV =   Simian Cytomegalovirus Promoter Region
SP =   Heavy Chain Signal Peptide
HC =   Mu Heavy Chain Gene
IRES =   Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide
LC=   Kappa or Lambda Light Chain Gene
RESE =   RNA Export and Stability Element
LTR =   Moloney Murine Leukemia Virus Long Terminal Repeat

GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCAT
AGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCA
GTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATG
GCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGG
GAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCC
CATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
TAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCG
GGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGT
TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGG
GGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTAT
GCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAA
CTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGC
CGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGC
TTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
TGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
CACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACC
AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
TTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAA
GATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAG
CCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGAC

FIGURE 21(B)

CCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCCGA
TCTGATCAAGAGACAGGATGAGAAGTCAAGATGAAGAACCATTTGCTTTTCTGGGGAGT
CCTGGCGGTTTTTATTAAGGCTGTTCATGTGAAAGCCCAAGAAGATGAAAGGATTGTTC
TTGTTGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTTCCGAA
GATCCTAATGAGGACATTGTGGAGAGAAACATCCGAATTATTGTTCCTCTGAACAACAG
GGAGAATATCTCTGATCCCACCTCACCATTGAGAACCAGATTTGTGTACCATTTGTCTG
ACCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCT
ACCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAG
AAACAAGTGCTACACAGCTGTGGTCCCACTCGTATATGGTGGTGAGACCAAAATGGTGG
AAACAGCCTTAACCCCAGATGCCTGCTATCCTGACTAAGATCCCTATGGCTATTGGCCA
GGTTCAATACTATGTATTGGCCCTATGCCATATAGTATTCCATATATGGGTTTTCCTAT
TGACGTAGATAGCCCCTCCCAATGGGCGGTCCCATATACCATATATGGGGCTTCCTAAT
ACCGCCCATAGCCACTCCCCCATTGACGTCAATGGTCTCTATATATGGTCTTTCCTATT
GACGTCATATGGGCGGTCCTATTGACGTATATGGCGCCTCCCCCATTGACGTCAATTAC
GGTAAATGGCCCGCCTGGCTCAATGCCCATTGACGTCAATAGGACCACCCACCATTGAC
GTCAATGGGATGGCTCATTGCCCATTCATATCCGTTCTCACGCCCCCTATTGACGTCAA
TGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATTAATAGTAACTTGGCAAGT
ACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGC
GGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAATGGGGAGGGGCA
ATGACGCAAATGGGCGTTCCATTGACGTAAATGGGCGGTAGGCGTGCCTAATGGGAGGT
CTATATAAGCAATGCTCGTTTAGGGAACCGCCATTCTGCCTGGGGACGTCGGAGGAGCT
CGAAAGCTTAGGACCTCACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACA
GCTACAGGTGTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCACATATTGGA
TGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGATTGGAGAAATTCATCCA
GATAGCAGTACGATTAACTATGCGCCGTCTCTAAAGGATAGATTTACAATATCGCGAGA
CAACGCCAAGAACACATTGTTCCTGCAAATGGACAGCCTGAGACCCGAAGACACCGGGG
TCTATTTTTGTGCAAGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGG
ACCCCGGTCACCGTCTCCTCAGGGAGTGCATCCGCCCCAACCCTTTTCCCCCTCGTCTC
CTGTGAGAATTCCCCGTCGGATACGAGCAGCGTGGCCGTTGGCTGCCTCGCACAGGACT
TCCTTCCCGACTCCATCACTTTGTCCTGGAAATACAAGAACAACTCTGACATCAGCAGT
ACCCGGGGGCTTCCCATCAGTCCTGAGAGGGGGCAAGTACGCAGCCACCTCACAGGTGCT
GCTGCCTTCCAAGGACGTCATGCAGGGCACAGACGAACACGTGGTGTGCAAAGTCCAGC
ACCCCAACGGCAACAAAGAAAGAACGTGCCTCTTCCAGTGATTGCCGAGCTGCCTCCC
AAAGTGAGCGTCTTCGTCCCACCCCGCGACGGCTTCTTCGGCAACCCCCGCAAGTCCAA
GCTCATCTGCCAGGCCACGGGTTTCAGTCCCCGGCAGATTCAGGTGTCCTGGCTGCGCG
AGGGGAAGCAGGTGGGGTCTGGCGTCACCACGGACCAGGTGCAGGCTGAGGCCAAAGAG
TCTGGGCCCACGACCTACAAGGTGACCAGCACACTGACCATCAAAGAGAGCGACTGGCT
CGGCCAGAGCATGTTCACCTGCCGCGTGGATCACAGGGGCCTGACCTTCCAGCAGAATG
CGTCCTCCATGTGTGTCCCCGATCAAGACACAGCCATCCGGGTCTTCGCCATCCCCCCA
TCCTTTGCCAGCATCTTCCTCACCAAGTCCACCAAGTTGACCTGCCTGGTCACAGACCT
GACCACCTATGACAGCGTGACCATCTCCTGGACCCGCCAGAATGGCGAAGCTGTGAAAA
CCCACACCAACATCTCCGAGAGCCACCCCAATGCCACTTTCAGCGCCGTGGGTGAGGCC
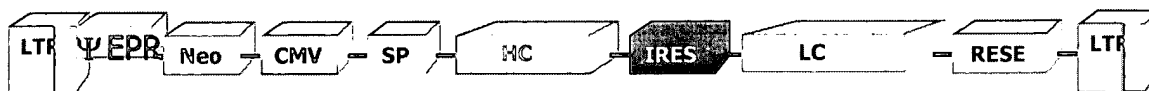AGCATCTGCGAGGATGACTGGAATTCCGGGGAGAGGTTCACGTGCACCGTGACCCACAC

FIGURE 21(C)

AGACCTGCCCTCGCCACTGAAGCAGACCATCTCCCGGCCCAAGGGGGTGGCCCTGCACA
GGCCCGATGTCTACTTGCTGCCACCAGCCCGGGAGCAGCTGAACCTGCGGGAGTCGGCC
ACCATCACGTGCCTGGTGACGGGCTTCTCTCCCGCGGACGTCTTCGTGCAGTGGATGCA
GAGGGGGCAGCCCTTGTCCCCGGAGAAGTATGTGACCAGCGCCCCAATGCCTGAGCCCC
AGGCCCCAGGCCGGTACTTCGCCCACAGCATCCTGACCGTGTCCGAAGAGGAATGGAAC
ACGGGGGAGACCTACACCTGCGTGGCCCATGAGGCCCTGCCCAACAGGGTCACCGAGAG
GACCGTGGACAAGTCCACCGGTAAACCCACCCTGTACAACGTGTCCCTGGTCATGTCCG
ACACAGCTGGCACCTGCTACTGAGATCTCTGCAGAAACCGGTCCTAGGTTTGGGAATTC
GCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAA
AGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAA
GACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGG
TGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCA
GTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTAT
TCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGG
CCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCC
GAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTC
TCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCCAGCTGACCCA
GAGCCCAAGCAGCCTGAGCGCCAGCGTGGGTGACAGAGTGACCATCACCTGTAAGGCCA
GTCAGGATGTGGGTACTTCTGTAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAG
CTGCTGATCTACTGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAG
CGGTAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACATCGCCA
CCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAAGGGACCAAGGTGGAA
ATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT
GAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCA
AAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACA
GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGC
CCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGATCTGTTAACCCTAGGCTCGAGTT
CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTA
ACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCT
ATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCT
TTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTG
ACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTC
GCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTG
GACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGT
CCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGC
TACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCT
GCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCG
CCTCCCCGCATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGA
AAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG
AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGC
TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAA

FIGURE 21(D)

GAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGC
CCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCT
AGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTAT
TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCT
CAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGC
CCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCT
GTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT

Figure 22(A). Gene Sequence of a Double Retrovector IgM Heavy and Light Chain Construct (SEQ ID NO:38).

LTR =   Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat
             Fusion
Ψ EPR =   Moloney Murine Leukemia Virus Psi Region and Extended Viral
             Packaging Region
Neo =   Neomycin Resistance Gene
CMV =   Simian Cytomegalovirus Promoter Region
SP =   Heavy Chain Signal Peptide
HC =   Mu Heavy Chain Gene
IRES =   Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide
LC=   Kappa or Lambda Light Chain Gene
RESE =   RNA Export and Stability Element
LTR =   Moloney Murine Leukemia Virus Long Terminal Repeat

GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCAT
AGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCA
GTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATG
GCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGG
GAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCC
CATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
TAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCG
GGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGT
TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGG
GGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTAT
GCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAA
CTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGC
CGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGC
TTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
TGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
CACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACC
AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
TTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAA

FIGURE 22(B)

GATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAG
CCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGAC
CCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCCGA
TCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGC
AGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAA
TCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTT
GTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATC
GTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTT
GCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGA
TCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
GGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCG
CCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGT
GACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGAT
TCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACC
CGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGG
TATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
GAGGATCCCTATGGCTATTGGCCAGGTTCAATACTATGTATTGGCCCTATGCCATATAG
TATTCCATATATGGGTTTTCCTATTGACGTAGATAGCCCCTCCCAATGGGCGGTCCCAT
ATACCATATATGGGGCTTCCTAATACCGCCCATAGCCACTCCCCCATTGACGTCAATGG
TCTCTATATATGGTCTTTCCTATTGACGTCATATGGGCGGTCCTATTGACGTATATGGC
GCCTCCCCCATTGACGTCAATTACGGTAAATGGCCCGCCTGGCTCAATGCCCATTGACG
TCAATAGGACCACCCACCATTGACGTCAATGGGATGGCTCATTGCCCATTCATATCCGT
TCTCACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATA
TCTATTAATAGTAACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGC
AGTACTCCCATTGACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCC
CATTGACGTCAATGGGGAGGGGCAATGACGCAAATGGGCGTTCCATTGACGTAAATGGG
CGGTAGGCGTGCCTAATGGGAGGTCTATATAAGCAATGCTCGTTTAGGGAACCGCCATT
CTGCCTGGGGACGTCGGAGGAGCTCGAAAGCTTAGGACCTCACCATGGGATGGAGCTGT
ATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTCCGAGGTCCAACTGGTGGA
GAGCGGTGGAGGTGTTGTGCAACCTGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTG
GCTTCGATTTCACCACATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTT
GAGTGGATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCTAAA
GGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCCTGCAAATGGACA
GCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCAAGCCTTTACTTCGGCTTCCCC
TGGTTTGCTTATTGGGGCCAAGGGACCCCGGTCACCGTCTCCTCAGGGAGTGCATCCGC
CCCAACCCTTTTCCCCCTCGTCTCCTGTGAGAATTCCCCGTCGGATACGAGCAGCGTGG
CCGTTGGCTGCCTCGCACAGGACTTCCTTCCCGACTCCATCACTTTGTCCTGGAAATAC
AAGAACAACTCTGACATCAGCAGTACCCGGGGCTTCCCATCAGTCCTGAGAGGGGGCAA
GTACGCAGCCACCTCACAGGTGCTGCTGCCTTCCAAGGACGTCATGCAGGGCACAGACG
AACACGTGGTGTGCAAAGTCCAGCACCCCAACGGCAACAAAGAAAGAACGTGCCTCTT
CCAGTGATTGCCGAGCTGCCTCCCAAAGTGAGCGTCTTCGTCCCACCCCGCGACGGCTT
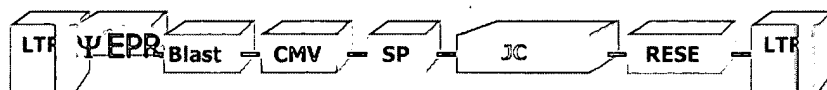CTTCGGCAACCCCCGCAAGTCCAAGCTCATCTGCCAGGCCACGGGTTTCAGTCCCCGGC

FIGURE 22(C)

AGATTCAGGTGTCCTGGCTGCGCGAGGGGAAGCAGGTGGGGTCTGGCGTCACCACGGAC
CAGGTGCAGGCTGAGGCCAAAGAGTCTGGGCCCACGACCTACAAGGTGACCAGCACACT
GACCATCAAAGAGAGCGACTGGCTCGGCCAGAGCATGTTCACCTGCCGCGTGGATCACA
GGGGCCTGACCTTCCAGCAGAATGCGTCCTCCATGTGTGTCCCCGATCAAGACACAGCC
ATCCGGGTCTTCGCCATCCCCCCATCCTTTGCCAGCATCTTCCTCACCAAGTCCACCAA
GTTGACCTGCCTGGTCACAGACCTGACCACCTATGACAGCGTGACCATCTCCTGGACCC
GCCAGAATGGCGAAGCTGTGAAAACCCACACCAACATCTCCGAGAGCCACCCCAATGCC
ACTTTCAGCGCCGTGGGTGAGGCCAGCATCTGCGAGGATGACTGGAATTCCGGGGAGAG
GTTCACGTGCACCGTGACCCACACAGACCTGCCCTCGCCACTGAAGCAGACCATCTCCC
GGCCCAAGGGGGTGGCCCTGCACAGGCCCGATGTCTACTTGCTGCCACCAGCCCGGGAG
CAGCTGAACCTGCGGGAGTCGGCCACCATCACGTGCCTGGTGACGGGCTTCTCTCCCGC
GGACGTCTTCGTGCAGTGGATGCAGAGGGGGCAGCCCTTGTCCCCGGAGAAGTATGTGA
CCAGCGCCCCAATGCCTGAGCCCCAGGCCCCAGGCCGGTACTTCGCCCACAGCATCCTG
ACCGTGTCCGAAGAGGAATGGAACACGGGGGAGACCTACACCTGCGTGGCCCATGAGGC
CCTGCCCAACAGGGTCACCGAGAGGACCGTGGACAAGTCCACCGGTAAACCCACCCTGT
ACAACGTGTCCCTGGTCATGTCCGACACAGCTGGCACCTGCTACTGAGATCTCTGCAGA
AACCGGTCCTAGGTTTGGGAATTCGCCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCC
GAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATATTG
CCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCC
TAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGGAAG
CAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAG
CGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC
ACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
TCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCC
CATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAG
GTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACAC
GATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCAC
CCAGGCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGTGACA
GAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGTAGCCTGGTACCAG
CAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACTGGACATCCACCCGGCACACTGG
TGTGCCAAGCAGATTCAGCGGTAGCGGTAGCGGTACCGACTTCACCTTCACCATCAGCA
GCCTCCAGCCAGAGGACATCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCG
TTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA
ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCG
GGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG
TCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG
ATCTGTTAACCCTAGGCTCGAGTTCGACATCGATAATCAACCTCTGGATTACAAAATTT
GTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCT
GCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTT
GTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTG
GCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACC
TGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCAT

FIGURE 22(D)

CGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCG
TGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGG
ATTCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCC
TTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGA
CGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATAAAATAAAAGATTTTATTTA
GTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAA
GTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATC
AAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGG
ATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGAT
GCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGG
ACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGT
TCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
CAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAG
TTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTA
CCCGTCAGCGGGGGTCTTTCATT

Figure 23(A) Gene Sequence of a Double Retrovector IgM J Chain Construct (SEQ ID NO:39).

LTR =   Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat
               Fusion
Ψ EPR =   Moloney Murine Leukemia Virus Psi Region and Extended Viral
               Packaging Region
Blast =   Blasticidin Resistance Gene
CMV =   Simian Cytomegalovirus Promoter Region
SP =   J Chain Signal Peptide
JC =   J Chain Gene
RESE =   RNA Export and Stability Element
LTR =   Moloney Murine Leukemia Virus Long Terminal Repeat

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GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCAT
AGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGGCA
GTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATG
GCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACA
TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGG
CGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGG
GAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCC
CATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
TAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCG
GGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGT
TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGG
GGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTAT
GCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAA
CTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGC
CGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGC
TTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
TGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
CACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACC
AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
TTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACGAGACCTCATCACCCAGGTTAA
GATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAG
CCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGAC
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FIGURE 23(B)

CCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCATG
GCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAA
CAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGCC
GCATCTTCACTGGTGTCAATGTATATCATTTTACTGGGGGACCTTGTGCAGAACTCGTG
GTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGG
AAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCTCGATC
TGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTTGGG
ATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTTGGATCCCTATG
GCTATTGGCCAGGTTCAATACTATGTATTGGCCCTATGCCATATAGTATTCCATATATG
GGTTTTCCTATTGACGTAGATAGCCCCTCCCAATGGGCGGTCCCATATACCATATATGG
GGCTTCCTAATACCGCCCATAGCCACTCCCCCATTGACGTCAATGGTCTCTATATATGG
TCTTTCCTATTGACGTCATATGGGCGGTCCTATTGACGTATATGGCGCCTCCCCCATTG
ACGTCAATTACGGTAAATGGCCCGCCTGGCTCAATGCCCATTGACGTCAATAGGACCAC
CCACCATTGACGTCAATGGGATGGCTCATTGCCCATTCATATCCGTTCTCACGCCCCCT
ATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATTAATAGTA
ACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTG
ACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAAT
GGGGAGGGGCAATGACGCAAATGGGCGTTCCATTGACGTAAATGGGCGGTAGGCGTGCC
TAATGGGAGGTCTATATAAGCAATGCTCGTTTAGGGAACCGCCATTCTGCCTGGGGACG
TCGGAGGAGCTCGAAAGCTTGAAGTCAAGATGAAGAACCATTTGCTTTTCTGGGGAGTC
CTGGCGGTTTTTATTAAGGCTGTTCATGTGAAAGCCCAAGAAGATGAAAGGATTGTTCT
TGTTGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTTCCGAAG
ATCCTAATGAGGACATTGTGGAGAGAAACATCCGAATTATTGTTCCTCTGAACAACAGG
GAGAATATCTCTGATCCCACCTCACCATTGAGAACCAGATTTGTGTACCATTTGTCTGA
CCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCTA
CCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAGA
AACAAGTGCTACACAGCTGTGGTCCCACTCGTATATGGTGGTGAGACCAAAATGGTGGA
AACAGCCTTAACCCCAGATGCCTGCTATCCTGACTAAGATCTGTTAACCGGTCCTAGGT
TTAAACTCGAGTTCGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTG
ACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCC
TTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCT
GGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGC
ACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCT
TTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCC
TTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCG
GGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGG
GACGTCCTTCTGCTACGTCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCC
TGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATC
TCCCTTTGGGCCGCCTCCCCGCATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAA
AAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATT
TTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAA
CAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCC
GGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT

FIGURE 23(C)

AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGA
CCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
TGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGA
TTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGAC
TTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGG
GGGTCTTTCATT

FIGURE 24(A)

Mouse dihydrofolate reductase retrovector gene construct (SEQ ID NO:40).

LTR =   Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat
               Fusion
Ψ EPR =   Moloney Murine Leukemia Virus Psi Region and Extended Viral
               Packaging Region
DHFR =   Mouse Dihydrofolate Reductase Gene
CMV =   Simian Cytomegalovirus Promoter Region
MCS=   Multiple Cloning Site (Gene Insertion Site)
RESE =   RNA Export and Stability Element
LTR =   Moloney Murine Leukemia Virus Long Terminal Repeat

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  1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTC
    ATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
    CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCC
    AATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGG
    CAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAA
    TGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTA
    CATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATG
    GGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
    GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGC
    CCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTC
    AATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCC
    CGGGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCT
    GTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTG
    GGGGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
    TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTT
    ATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGG
    AACTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGG
    GCCGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGA
    TATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTT
    GCTTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
    TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTT
    ACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
    CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAA
    CCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTT
    AAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGT
    GACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTA
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FIGURE 24(B)

AGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCG
ACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCC
GATCTGATCAAGAGACAGGATGACCTAGGCTTTTGCAAAAAGCTTTATCCCCGCTGCCA
TCATGGTTCGACCATTGAACTGCATCGTCGCCGTGTCCCAAGATATGGGGATTGGCAAG
AACGGAGACCTACCCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGAC
CACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGT
TCTCCATTCCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTTCTCAGTAGA
GAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGCCAAAGTTTGGATGATGCCTT
AAGACTTATTGAACAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAG
GCAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTCAGACTCTTTGTGACA
AGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTGGGGAAATA
TAAACTTCTCCCAGAATACCCAGGCGTCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCA
AGTATAAGTTTGAAGTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCT
GCTCCCCTCCTAAAGCTATGCATTTTTATAAGACCATGGGACTTTTGCTGGCTTTAGAT
CCCTATGGCTATTGGCCAGGTTCAATACTATGTATTGGCCCTATGCCATATAGTATTCC
ATATATGGGTTTTCCTATTGACGTAGATAGCCCCTCCCAATGGGCGGTCCCATATACCA
TATATGGGGCTTCCTAATACCGCCCATAGCCACTCCCCCATTGACGTCAATGGTCTCTA
TATATGGTCTTTCCTATTGACGTCATATGGGCGGTCCTATTGACGTATATGGCGCCTCC
CCCATTGACGTCAATTACGGTAAATGGCCCGCCTGGCTCAATGCCCATTGACGTCAATA
GGACCACCCACCATTGACGTCAATGGGATGGCTCATTGCCCATTCATATCCGTTCTCAC
GCCCCCTATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATATCTATT
AATAGTAACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACT
CCCATTGACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGA
CGTCAATGGGGAGGGGCAATGACGCAAATGGGCGTTCCATTGACGTAAATGGGCGGTAG
GCGTGCCTAATGGGAGGTCTATATAAGCAATGCTCGTTTAGGGAACCGCCATTCTGCCT
GGGGACGTCGGAGGAGCTCGAAAGCTTCTAGACAATTGACGCGTAGGCCTGCGGCCGCG
TCGACCAAGGGCCCAGATCTGTTAACCGGTCCTAGGTTTAAACTCGAGTTCGACATCGA
TAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTG
CTCCTTTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCC
CGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGA
GTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCC
CCACTGGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTTCCCC
CTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGC
TCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTT
GGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCCT
TCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCT
TCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGC
ATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA
CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACA
TAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGG
GCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATG
GAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCA
GGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCA

FIGURE 24(C)

TCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAA
CCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAG
AGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACC
CGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGG
GAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT   4354

    1 -   763   HCMV-MOMUSV CHIMERIC 5'LTR
  833 - 1642   EXTENDED PACKAGING REGION
 1712 - 2272   MOUSE DHFR GENE CODING REGION
 2355 - 3038   SIMIAN CMV PROMOTER
 3029 - 3114   MULTIPLE CLONING SITE (SITE OF GENE
                    INSERTION)
 3121 - 3721   RESE
 3761 - 4354   3'LTR

Figure 25(A)

Glutamine synthase Retrovector gene construct (SEQ ID NO:41)

LTR =   Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat
               Fusion
Ψ EPR =   Moloney Murine Leukemia Virus Psi Region and Extended Viral
               Packaging Region
DHFR =   Mouse Glutamine Synthase Gene
CMV =   Simian Cytomegalovirus Promoter Region
MCS=   Multiple Cloning Site (Gene Insertion Site)
RESE =   RNA Export and Stability Element
LTR =   Moloney Murine Leukemia Virus Long Terminal Repeat

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1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTC
ATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCC
AATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCCACTTGG
CAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAA
TGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTA
CATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATG
GGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGC
CCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTC
AATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCC
CGGGTACCCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCT
GTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTG
GGGGCTCGTCCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTT
ATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGG
AACTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGG
GCCGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGA
TATGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTT
GCTTTCGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTT
ACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAA
CCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTT
AAGATCAAGGTCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGT
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FIGURE 25(B)

GACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTA
AGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCG
ACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCC
GATCTGATCAAGAGACAGGATGAACCATGGCCACCTCAGCAAGTTCCCACTTGAACAAA
GGCATCAAGCAAATGTACATGTCCCTGCCCCAGGGTGAGAAAGTCCAAGCCATGTATAT
CTGGGTTGATGGTACCGGAGAAGGACTGCGCTGCAAGACCCGTACCCTGGACTGTGAGC
CCAAGTGTGTGGAAGAGTTACCTGAGTGGAACTTTGATGGCTCTAGTACCTTTCAGTCT
GAAGGCTCCAACAGCGACATGTACCTCCATCCTGTTGCCATGTTTCGAGACCCCTTCCG
CAAAGACCCCAACAAGCTGGTGCTATGTGAAGTTTTCAAGTATAACCGGAAGCCTGCAG
AGACCAACTTGAGGCACATCTGTAAACGGATAATGGACATGGTGAGCAACCAGCACCCC
TGGTTTGGAATGGAGCAGGAATATACTCTTATGGGAACAGACGGCCACCCATTTGGTTG
GCCTTCCAATGGCTTCCCTGGACCCCAAGGCCCGTATTACTGCGGTGTGGGAGCAGACA
AGGCCTACGGCAGGGACATCGTGGAGGCTCACTACCGGGCCTGCTTGTATGCTGGAGTC
AAGATCACGGGGACAAATGCGGAGGTTATGCCTGCCCAGTGGGAATTCCAGATAGGACC
CTGTGAGGGGATCCGAATGGGAGATCATCTTTGGATAGCCCGTTTTATCTTGCATCGGG
TGTGCGAAGACTTTGGGGTGATAGCAACCTTTGACCCCAAGCCCATTCCAGGGAACTGG
AATGGTGCAGGCTGCCATACCAACTTCAGCACCAAGGCCATGCGGGAGGAGAATGGTCT
GAAGTGCATTGAGGAGGCCATTGACAAACTGAGCAAGAGGCACCAGTACCACATCCGCG
CCTACGATCCCAAGGGGGGCCTGGACAACGCCCGGCGTCTGACTGGATTCCACGAAACC
TCCAACATCAACGACTTTTCTGCCGGTGTTGCCAACCGCGGTGCCAGTATCCGCATTCC
CCGGACTGTCGGCCAGGAGAAGAAGGGCTACTTTGAAGACCGTCGGCCTTCTGCCAATT
GTGACCCCTATGCGGTGACAGAAGCCATCGTCCGCACGTGTCTCCTCAACGAAACAGGC
GACGAACCCTTCCAATACAAGAACTAAGGATCCCTATGGCTATTGGCCAGGTTCAATAC
TATGTATTGGCCCTATGCCATATAGTATTCCATATATGGGTTTTCCTATTGACGTAGAT
AGCCCCTCCCAATGGGCGGTCCCATATACCATATATGGGGCTTCCTAATACCGCCCATA
GCCACTCCCCCATTGACGTCAATGGTCTCTATATATGGTCTTTCCTATTGACGTCATAT
GGGCGGTCCTATTGACGTATATGGCGCCTCCCCCATTGACGTCAATTACGGTAAATGGC
CCGCCTGGCTCAATGCCCATTGACGTCAATAGGACCACCCACCATTGACGTCAATGGGA
TGGCTCATTGCCCATTCATATCCGTTCTCACGCCCCCTATTGACGTCAATGACGGTAAA
TGGCCCACTTGGCAGTACATCAATATCTATTAATAGTAACTTGGCAAGTACATTACTAT
TGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGCGGTAAATGGC
CCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAATGGGGAGGGGCAATGACGCAAA
TGGGCGTTCCATTGACGTAAATGGGCGGTAGGCGTGCCTAATGGGAGGTCTATATAAGC
AATGCTCGTTTAGGGAACCGCCATTCTGCCTGGGGACGTCGGAGGAGCTCGAAAGCTTC
TAGACAATTGACGCGTAGGCCTGCGGCCGCGTCGACCAAGGGCCCAGATCTGTTAACCG
GTCCTAGGTTTAAACTCGAGTTCGACATCGATAATCAACCTCTGGATTACAAAATTTGT
GAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGC
TTTAATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGT
ATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGC
GTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTG
TCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCATCG
CCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTG
GTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT

FIGURE 25(C)

TCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTT
CCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACG
AGTCGGATCTCCCTTTGGGCCGCCTCCCCGCATCGATAAAATAAAAGATTTTATTTAGT
CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGT
AACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAA
GGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGT
TCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGAT
ATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGC
GGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC
CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTC
GCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCA
GTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTT
GCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACC
CGTCAGCGGGGGTCTTTCATT 4797

       1 -   763   HCMV-MOMUSV CHIMERIC 5'LTR
     833 - 1642   EXTENDED PACKAGING REGION
    1677 - 2795   MOUSE GLUTAMINE SYNTHASE GENE
                      CODING REGION
    2805 - 3472   SIMIAN CMV PROMOTER
    3473 - 3558   MULTIPLE CLONING SITE (SITE OF GENE
                      INSERTION)
    3565 - 4165   RESE
    4205 - 4797   3'LTR